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A new species of the genus *Ptyctolaemus* Peters, 1864 (Squamata, Agamidae) from Sagaing, Myanmar

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Abstract

A new species of *Ptyctolaemus* Peters, 1864 is described from Htamanthi Wildlife Sanctuary, Sagaing Division, Myanmar. The new species differs from *P. gularis* and *Ptyctolaemus* aff. *gularis* from Tibet, China, by having relatively longer limbs and different colorations of the gular region, and it differs from *P. collicristatus* by having much longer limbs and a less developed nuchal crest in males. Moreover, the new species differs genetically from *Ptyctolaemus* aff. *gularis* from Tibet, China, and *P. collicristatus* by an uncorrected percentage distance of 23.5% and 24.8%, respectively, inferred from mitochondrial NADH dehydrogenase subunit 2 gene sequences. This discovery increases the number of known *Ptyctolaemus* species to three.

Key Words

Htamanthi Wildlife Sanctuary, morphology, ND2, phylogeny, systematics, taxonomy

Introduction

The agamid genus *Ptyctolaemus* Peters, 1864 is characterized by the males having longitudinal parallel folds on either side of the throat (Peters 1864; Ananjeva and Stuart 2001; Schulte et al. 2004). *Ptyctolaemus* currently contains two species: *P. gularis* (Peters, 1864) and *P. collicristatus* Schulte & Vindum, 2004. *Mantheyus phuwuanensis* (Manthey & Nabhitabhata, 1991), a species which once also was assigned to *Ptyctolaemus* due to the presence of folds on either side of the throat (Manthey and Nabhitabhata 1991; Hallermann and Böhme 2003), is currently assigned to a monotypic genus (Ananjeva and Stuart 2001; Schulte et al. 2004; Uetz et al. 2021).

The type locality of *P. gularis* is not certain as the type specimen was purchased from Calcutta, India (Peters 1864; Jerdon 1870), but this species is thought to be widely distributed in northeastern India, Bhutan, southwest China, Bangladesh, and northern Myanmar (Smith 1940; Huang 1980; Mathew 1995; Ananjeva and Stuart 2001; Pawar and Birand 2001; Schulte et al. 2004; Ahsan et al. 2008; Ahmed et al. 2009; Manthey 2010; Purkayastha 2013, 2018; Das et al. 2014, 2016; Che et al. 2020; Hakim et al. 2020; Khandekar et al. 2021; Uetz et al. 2021). *Ptyctolaemus collicristatus* is currently known only from Chin State, western Myanmar (Schulte et al. 2004; Manthey 2010; Uetz et al. 2021).

In China, *Ptyctolaemus gularis* was recorded from Beibeng Township, Medog, Tibet by Huang (1980) and Che et al. (2020). In Myanmar, *P. gularis* was recorded from Kachin State (Smith 1940) and Sagaing Division (Schulte et al. 2004).

During our fieldwork in northern Myanmar in 2019, four specimens of *Ptyctolaemus* cf. *gularis* were collected from Htamanthi Wildlife Sanctuary, Sagaing Division, Myanmar. Morphological and molecular data of these specimens showed obvious differences from the data of the specimens from Tibet, China recorded by Huang (1980) and Che et al. (2020). As no molecular data are available for the type specimen of *P. gularis*, after comparing the

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morphological data (Huang 1980; Che et al. 2020) of the specimens from Tibet, China, and the morphological data of our newly collected specimens with the morphological data (Schulte et al. 2004) of the type specimen (holotype ZMB 5004) of *P. gularis*, we found that the specimens from Tibet, China, largely agree with the type specimen but that the newly collected specimens disagree with the type specimen. Therefore, we consider the specimens from Tibet, China, as *Ptyctolaemus* aff. *gularis* and describe the specimens from Sagaing, Myanmar, as a new species herein.

Materials and methods

Field surveys in northern Myanmar were undertaken at the invitation of the Republic of the Union of Myanmar, Ministry of Natural Resources and Environmental Conservation, Forest Department, Forest Research Institute. Specimens were collected by hand at night from Htamanthi Wildlife Sanctuary, Sagaing Division, Myanmar, in December 2019. Photographs were taken to document the color pattern in life prior to euthanasia. Liver tissues were stored in 99% ethanol and lizards were preserved in 75% ethanol. Specimens were deposited in Southeast Asia Biodiversity Research Institute, Chinese Academy of Sciences (abbreviation: SEABRI; address: Yezin, Nay Pyi Taw, Myanmar).

Genomic DNA was extracted from preserved liver tissues using a standard phenol-chloroform extraction protocol (Sambrook et al. 1989). A fragment of the mitochondrial gene NADH dehydrogenase subunit 2 (ND2) gene was amplified and sequenced by using the primers L4437b: AAGCAGTTGGGCCCATACC and H5540: TTTAGGGCTTTGAAGGC (Macey et al. 2000). PCR was conducted using a denaturing step at 94 °C for 35 s, annealing at 55 °C for 35 s, and extending at 70 °C for 150 s. PCR products were electrophoresed in 1.5% agarose gels, visualized with ethidium bromide. The products were purified and sequenced Tsingke Biotechnology (Beijing) Co., Ltd., using the same primers as in PCR. Sequences were edited and manually managed using SeqMan in Lasergene 7.1 (DNASTAR Inc., Madison, WI, USA) and MEGA X (Kumar et al. 2018). All new sequences were deposited in GenBank. *Draco blanfordii* Boulenger, *Japalura tricarinata* (Blyth), *Calotes calotes* (Linnaeus), and *Mantheyus phuwuanensis* were chosen as outgroups based on Schulte et al. (2004) and Che et al. (2020). Homologous and outgroup sequences were obtained from GenBank (Table 1).

Sequences were aligned using ClustalW (Thompson et al. 2002) with default parameters in MEGA X (Kumar et al. 2018) with default parameters. The genetic divergence (uncorrected p-distance) between species was calculated in MEGA X (Kumar et al. 2018). The best substitution model GTR+F+I+G4 was selected using the Akaike Information Criterion (AIC) in ModelFinder (Kalyaanamoorthy et al. 2017). Bayesian Inference was performed in MrBayes 3.2.6 (Ronquist et al. 2012). Two runs were performed simultaneously with four Markov chains Monte Carlo (MCMC) simulations, three hot and one cold. The chains were run for 10,000,000 generations and sampled every 1,000 generations. The first 25% of sampled trees were discarded as burn-in. Chain stationarity and run parameter convergence were checked in Tracer 1.7.1 (Rambaut et al. 2018). Maximum Likelihood analysis was performed in raxmlGUI 2.0 (Silvestro and Michalak 2012) and nodal support was estimated by 1,000 rapid bootstrap replicates.

Measurements were taken with a digital caliper to the nearest 0.1 mm, except tail length (TAL) which was measured using a string and a ruler. Morphological terminology followed Schulte et al. (2004) and Che et al. (2020). Paired meristic characters are given as left/right. Morphometric characters included: FLL, forelimb length, from forelimb insertion to end of fourth finger; HL, head length, distance from tip of snout to rear border of right angle of jaw; HLL, hindlimb length, from thigh insertion to end of fourth toe; HW, head width, widest point in the temporal region, anterior to the tympanum; InfL, Infralabials, number of enlarged scales bordering left and right margin of lower lip (not including mental scale); IOD, interorbital distance; MB, number of scales around midbody; NC, number of nuchal crest spines, enlarged mid-dorsal crest scales from posterior portion of the head to the posterior portion of the nape; OD, orbit diameter, measured from the posterior to the anterior edge of the orbit; SEL, snout to eye length, measured from the anterior edge of orbit to the tip of snout; SupL, supralabials,

Table 1. Sequences used in this study.

Species	Locality	Voucher	GenBank
Ptyctolaemus chindwinensis sp. nov.	Htamanthi, Sagaing, Myanmar	SEABRI 2019120076	OK563731
Ptyctolaemus chindwinensis sp. nov.	Htamanthi, Sagaing, Myanmar	SEABRI 2019120016	OK563732
Ptyctolaemus chindwinensis sp. nov.	Htamanthi, Sagaing, Myanmar	SEABRI 2019120031	OK563733
Ptyctolaemus chindwinensis sp. nov.	Htamanthi, Sagaing, Myanmar	SEABRI 2019120046	OK563734
Ptyctolaemus collicristatus	Min Dat, Chin, Myanmar	USNM 559811	AY555837
Ptyctolaemus aff. *gularis*	Medog, Tibet, China	KIZ 016452	MK001393
Ptyctolaemus aff. *gularis*	Medog, Tibet, China	KIZ 06654	MW111456
Ptyctolaemus aff. *gularis*	Medog, Tibet, China	KIZ 09947	MW133374
Ptyctolaemus sp.	Putao, Kachin, Myanmar	CAS 221515	AY555838
Calotes calotes	Navinna, Galle, Sri Lanka	WHT 1679	AF128482
Draco blanfordii	An Khe, Gia Lai, Vietnam	MVZ 222156	AF128477
Japalura tricarinata	Zhangmu, Nyalam, Tibet, China	CAS 177397	AF128478
Mantheyus phuwuanensis	Thaphabat, Bolikhamxay, Laos	FMNH 255459	AY555836

number of enlarged scales bordering left and right margin of upper lip (not including rostral scale); SVL, snout-vent length; TAL, tail length; TRL, trunk length, distance between posterior edge of forelimb insertion to anterior edge of hindlimb insertion; T4L, fourth toe length, from base or fourth toe to toe tip; T4S, number of subdigital lamellae on the left and right fourth toe; VSR, number of ventral scale rows, scale rows between posterior margin of gular and anterior edge of vent; VT, Number of scales on the vertebral, counted at mid-dorsal first nuchal scale to the level directly above cloacal opening.

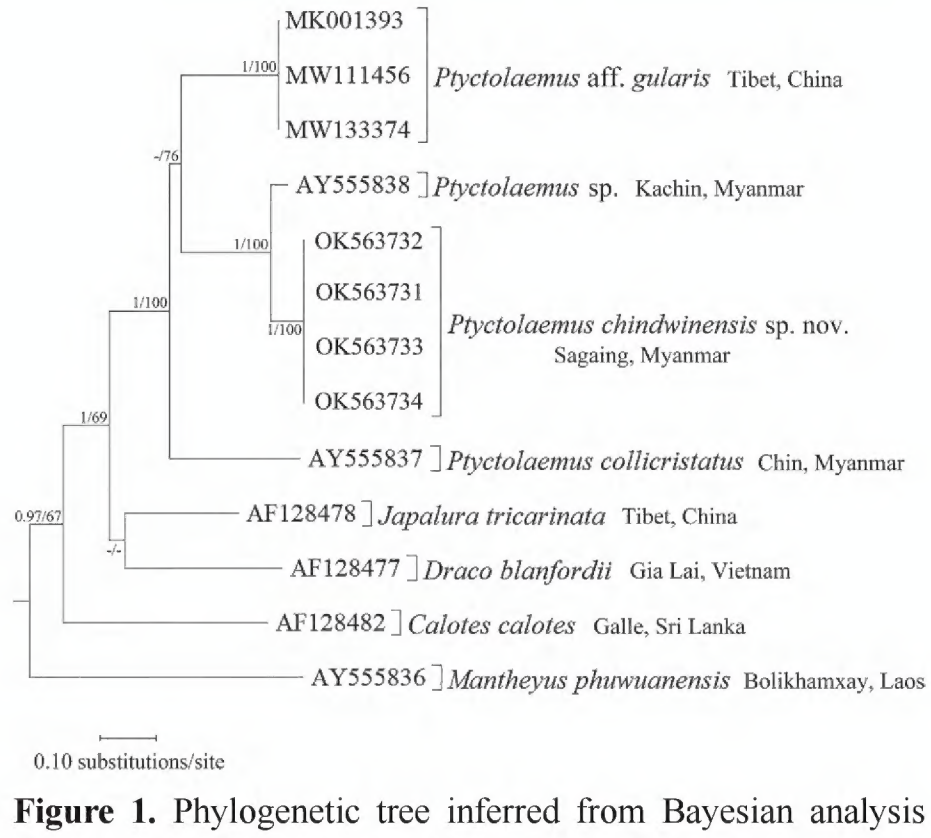

Figure 1. Phylogenetic tree inferred from Bayesian analysis based on the ND2 gene. Numbers before slashes indicate Bayesian posterior probabilities (only values above 0.9 are shown) and numbers after slashes indicate bootstrap support from Maximum Likelihood analysis (only values above 60 are shown).

Table 2. Genetic divergence (uncorrected p-distance) (%) among *Ptyctolaemus* and outgroups inferred from the ND2 gene sequences.

	1	2	3	4	5	6	7
1 *Ptyctolaemus chindwinensis* sp. nov. (n=4)							
2 *Ptyctolaemus collicristatus* (n=1)	24.8						
3 *Ptyctolaemus* aff. *Gularis* (n=3)	23.5	23.2					
4 *Ptyctolaemus* sp. (n=1)	8.1	23.2	22.5				
5 *Calotes calotes* (n=1)	30.9	30.2	31.1	29.3			
6 *Draco blanfordii* (n=1)	29.1	26.7	27.3	27.3	28.7		
7 *Japalura tricarinata* (n=1)	27.0	26.3	26.4	25.6	27.7	24.3	
8 *Mantheyus phuwuanensis* (n=1)	35.3	33.9	35.4	33.0	32.1	31.6	30.8

Results

The generated gene sequences were 1013 bp in length. The topologies derived from Bayesian Inference and Maximum Likelihood analyses were consistent (Fig. 1). The specimens from Sagaing, Myanmar, formed a separate clade sister to a specimen (CAS 221515) from Kachin, Myanmar, with strong support, and they together formed a clade sister to the specimens from Tibet, China, with weak support. The average uncorrected pairwise distance (p-distance) between the sequences of the specimens from Sagaing, Myanmar, and the sequences of the specimens from Tibet, China, is 23.5% (Table 2).

The gular regions of both sexes in life are white with long blue or bluish black stripes for the specimens from Tibet, China (Che et al. 2020), however, the gular regions of the males in life are bright yellow with short black stripes for the newly collected specimens from Sagaing, Myanmar (Fig. 6A–C), and the gular region of the female of the newly collected specimens in life is greyish white with no stripe (Fig. 6D).

Morphological comparisons are presented in Table 3. The specimens from Tibet, China, largely agree with the type specimen (Holotype ZMB 5004) of *Ptyctolaemus gularis*, there is a clear overlap in morphology of the specimens from Tibet, China, and the type specimen (Holotype ZMB 5004) of *P. gularis*. However, the ratios of FLL/SVL (0.48–0.52) and HLL/SVL (0.90–0.94) of the

Table 3. Comparisons of morphometric (in mm) and meristic data. Data for the holotype of *Ptyctolaemus gularis*, *Ptyctolaemus* cf. *gularis*, and *Ptyctolaemus* sp. were obtained from Schulte et al. (2004), data for *Ptyctolaemus* aff. *gularis* from Tibet were obtained from Huang (1980) and Che et al. (2020), and data for *Ptyctolaemus chindwinensis* sp. nov. were obtained from the new specimens (N=4) and Schulte et al. (2004) (N=1).

	Ptyctolaemus gularis **Holotype ZMB 5004 N=1 (♂)**	***Ptyctolaemus* aff. *gularis*** **Tibet, China N=6 (3♂, 3♀)**	***Ptyctolaemus* cf. *gularis*** **12 mi E Ledo, India; "N Chengyang, Myanmar" N=2 (1♂, 1♀)**	***Ptyctolaemus* sp. Other specimens identified as *P. gularis* in Schulte et al. (2004) N=20 (10♂, 10♀)**	***Ptyctolaemus chindwinensis*** **sp. nov. Sagaing, Myanmar N=5 (4♂, 1♀)**
SVL	65.7	63–70	56.1–75	45.1–81.5	45.6–87.4
TAL	153	147–176	124–177	100–209	102–213
TAL/SVL	2.33	2.26–2.51	2.21–2.36	2.22–2.63	2.24–2.47
HL	18.6	17.0–19.2	15.9–20.9	12.5–25	13.7–25.3
HW	10.9	9.1–10.1	9.2–10.9	7.5–12.9	8.6–13.7
HW/HL	0.58	0.52–0.55	0.52–0.58	0.48–0.69	0.54–0.63
HL/SVL	0.28	0.26–0.27	0.28	0.25–0.31	0.27–0.30
FLL	29.6	23.4–29.0	24.2–30.4	22.6–40.3	23.8–44.7
HLL	51.3	48.1–52.7	46.6–59	38.6–74.9	42.3–79.4
FLL/SVL	0.45	0.35–0.41	0.41–0.43	0.45–0.56	0.48–0.52
HLL/SVL	0.78	0.71–0.78	0.79–0.83	0.82–0.99	0.90–0.94
T4L	11.8	12.4–13.0	9.8–11.8	8.9–16.7	9.5–18.0
T4S	34	27–34	30	30–38	31–35
NC	24	24–27	16–18	14–24	26–30

specimens from Sagaing, Myanmar, are obviously greater than those (FLL/SVL 0.35–0.45; HLL/SVL 0.71–0.78) in the type specimen (Holotype ZMB 5004) of *P. gularis* and the specimens from Tibet, China. Therefore, we consider the specimens from Tibet, China, as *Ptyctolaemus* aff. *gularis* and the specimens from Sagaing, Myanmar, as a new species.

Ptyctolaemus chindwinensis sp. nov.

http://zoobank.org/DCB06863-25A1-4E8F-A8FF-714BBAC9707F

Figures 2–7

Ptyctolaemus gularis: Schulte et al. 2004 (partim): 222–247.

Holotype. SEABRI 2019120076, adult male, 16 December 2019. Nam E Zu section, Htamanthi Wildlife Sanctuary, Sagaing Division, Myanmar (25°25'57"N, 95°40'48"E, 180 m elevation).

Paratypes. SEABRI 2019120016, subadult male, 2 December 2019; SEABRI 2019120031, adult male, 5 December 2019; SEABRI 2019120046, adult female, 7 December 2019. All from Nam Pa Gon section, Htamanthi Wildlife Sanctuary, Sagaing Division, Myanmar (25°17'33"N, 95°33'26"E, 170 m elevation).

Etymology. The specific epithet refers to the Chindwin River, the new species was discovered in its basin.

Diagnosis. Body size medium, SVL 45.6–83.5 mm, slender, tail long, TAL/SVL 2.24–2.47, limbs long, FLL/SVL 0.48–0.52, HLL/SVL 0.90–0.94. Tympanum concealed. Nuchal crest undeveloped, low and flat. Dorsal scales heterogeneous. The gular region is bright yellow with two or three short black stripes in males and the gular region is greyish white with no stripe in females.

Description of the holotype. Adult male, habitus slender, slightly compressed laterally, SVL 83.5 mm, TAL 206 mm, TAL/SVL 2.47. Rostral scale crescent, width approximately 3.1 times of height, five scales in contact with rostral edge including the first supralabials; nasal octagonal, separated from rostral by one scale, seven scales in contact with nasal on each side; canthus rostralis sharp, composed of 12 enlarged scales on each side; scales on snout irregular in shape and size; an inverted Y-shaped pattern on the middle of the snout; ten supralabials left and eleven right; orbit 7.2 mm in horizontal diameter; distance from anterior edge of orbit to nostril 5.9 mm, and 9.6 mm to tip of rostral scale; tympanum concealed, covered with smooth, slightly imbricate scales, equal in size to adjacent scales; three enlarged scales posterior and horizontal to orbit, keeled and elevated; temporal area with three enlarged, pointing scales. Mental scale triangular, wider than long, slightly narrower than rostral; mental followed by an infralabial on either side and two postmentals in contact with first infralabials; posterior to postmentals are four chin shields on each side that run parallel to infralabials, anterior portion of first chin shield touching first infralabial, remaining portion of first chin shield and following two chin shields separated from infralabials by one scale row; nine infralabials left and ten right. Gular scales anterior to gular pouch small, rounded, imbricate and slightly mucronate; scales of gular pouch slightly keeled, becoming larger toward center. Nuchal crest poorly developed, composed of 29 conical scales. Scales from angle of jaw to shoulder with feebly keeled, imbricate scales, interspersed with three large pointed scales; small oblique curved fold in front of shoulder. Dorsal scales keeled, imbricate, pointing backwards; mid-dorsal scale row strongly keeled and equal in size to bordering dorsal scales, one row of discontinuous, strongly keeled, enlarged, scales net to the vertebral ridge, separated from the mid-dorsal scale row by three scale rows; lateral scales heterogeneous, majority of scales much smaller than dorsals, feebly keeled, imbricate, interspersed with enlarged strongly keeled scales; lateral scales pointing backwards and downwards. Ventral scales larger than lateral scales, approximately equal in size to largest dorsal scales, strongly keeled, imbricate, mucronate, pointing backwards. Limbs slender, covered dorsally with strongly keeled, imbricate, mucronate scales; ventral surface of limbs with smaller feebly keeled, imbricate, scales; relative length of digits: IV > III > II > V > I, relative length of toes: IV> III > V > II> I; 33/35 subdigital lamellae under fourth toes. Tail slightly compressed laterally, covered with homogenous, strongly keeled, imbricate, scales.

Color of holotype in life. Dorsal head light brownish grey, several indistinct transverse brown stripes on the anterior portion dorsally, two black spots on the top of the head; lateral head grayish brown, many indistinct radial black stripes around the eye, the two below and posterior to the eye extended to the corner of the mouth; ventral head grayish brown, gular region bright yellow with two horizontal parallel black stripes on the center of each side of the gular pouch, the lengths of the two stripes almost equal and no more than half length of the gular pouch, the two stripes slightly connected up and down, separated by a indistinct thin yellow stripe. Dorsal neck and body light brownish grey with some indistinct slightly symmetrical brown patches beside the vertebral ridge; lateral neck and body flank brownish grey with indistinct purple brown reticulated pattern; the middle of the ventral body white, ventrolateral region purple brown; dorsal side of the limbs brownish grey with some indistinct brown bands; ventral side of the limbs scattered with white and brown. Anterior portion of the tail brownish grey, middle portion of the tail with black and white rings, posterior portion of the tail almost uniform black.

Color of holotype in preservative. Dorsal head, neck, body, and limbs light brown, transverse stripes on dorsal head became more indistinct, the patches and bands on dorsal body and limbs almost invisible; lateral head light brown, the radial stripes around the eye still visible; lateral side of the neck grey; lateral side of the body brown, the reticulated pattern almost invisible; ventral side of the head, body, and limbs yellowish white, bright yellow on gular region faded; brown and white rings on the tail.

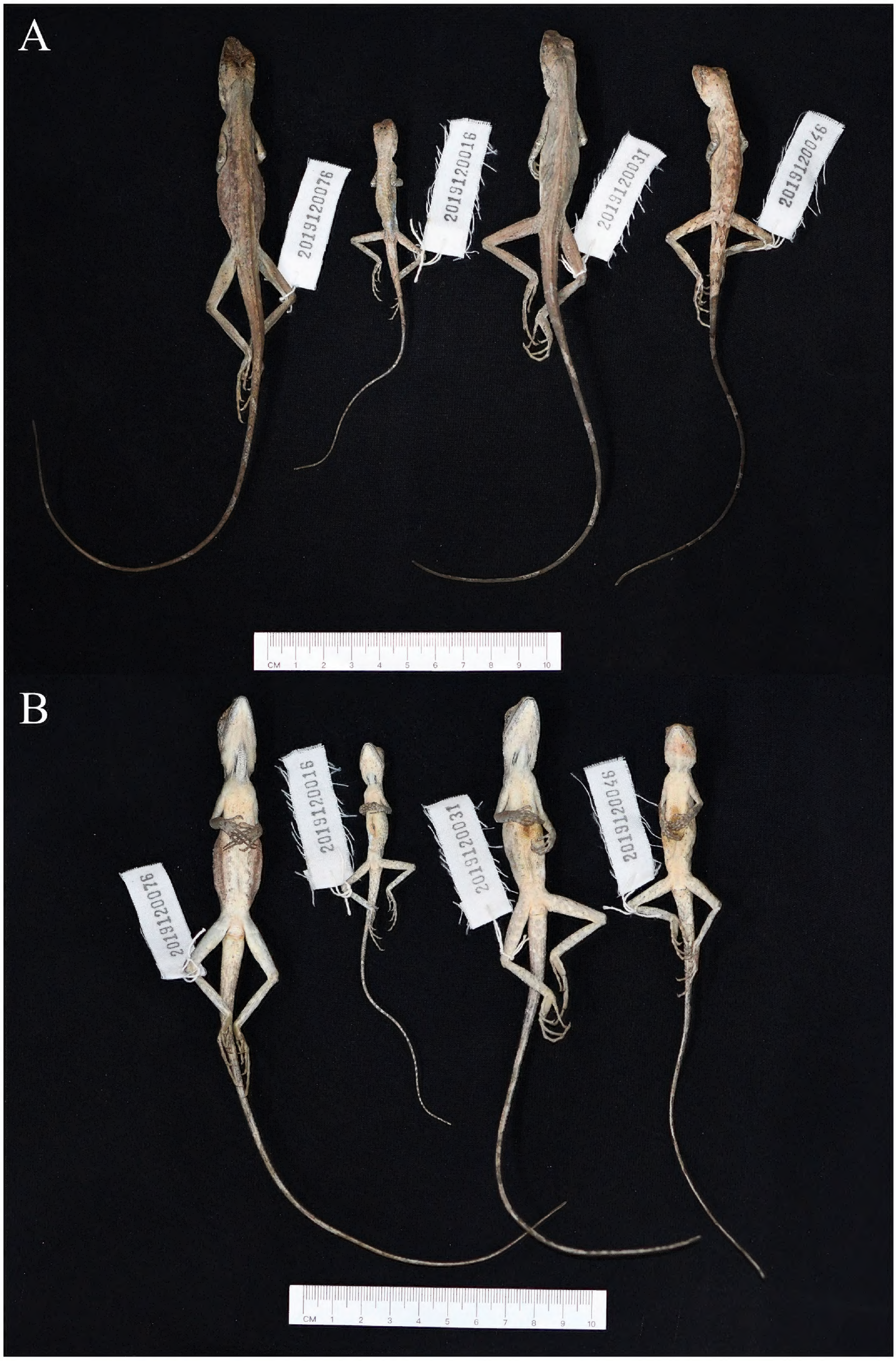

Figure 2. Type series of *Ptyctolaemus chindwinensis* sp. nov. in preservative. **A.** Dorsal view; **B.** Ventral view.

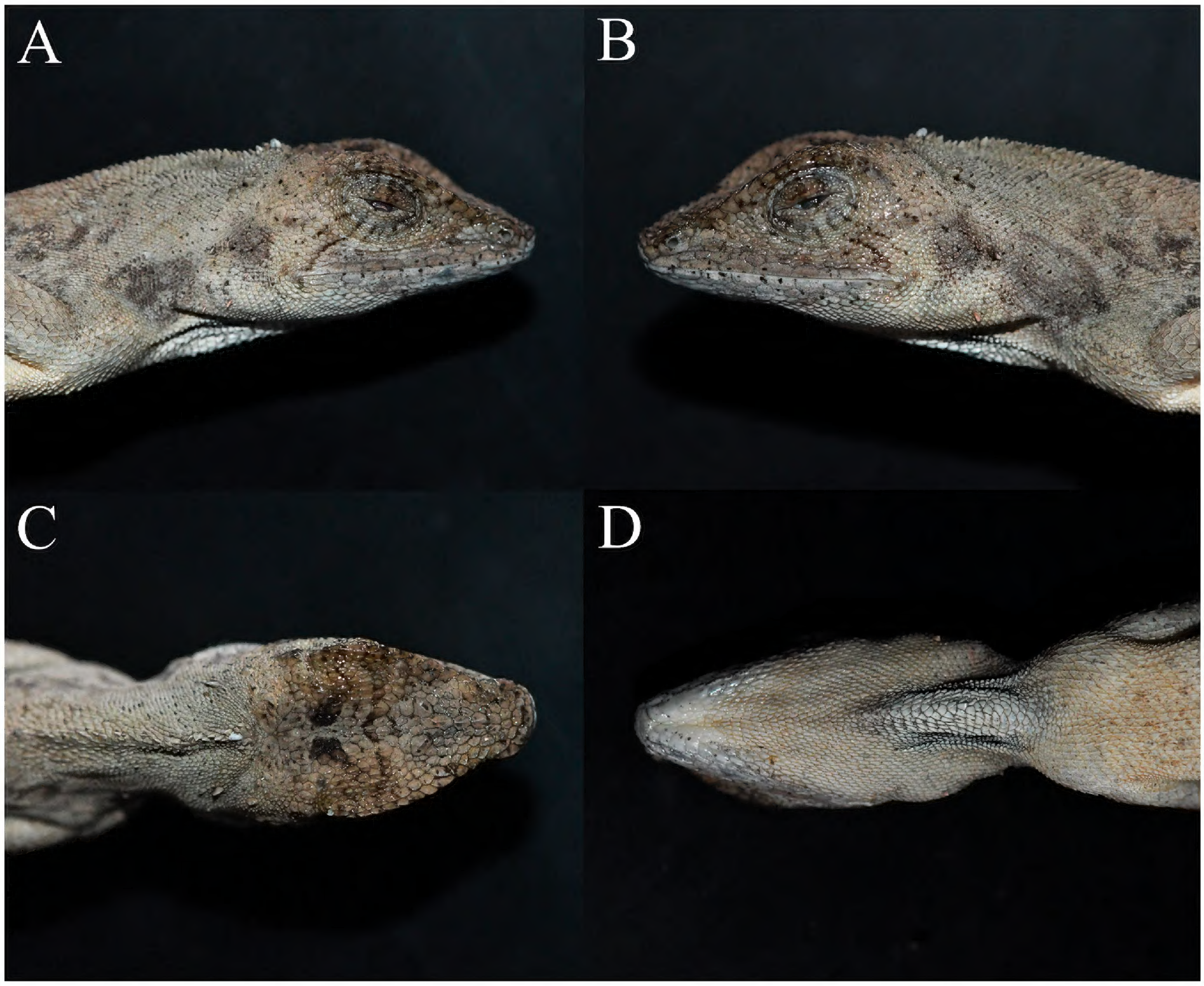

Figure 3. Head views of the holotype (SEABRI 2019120076) of *Ptyctolaemus chindwinensis* sp. nov. **A.** Right; **B.** Left; **C.** Dorsal; **D.** Ventral.

Variations. The paratypes resemble the holotype in morphometric characteristics, the paratypes merely having smaller body sizes than the holotype. For coloration, the male paratype (SEABRI 2019120031) has an almost uniform light brownish grey dorsal color with no stripes or patches, and the gular region has three black stripes, of which the upper two are parallel and the lower two intersect; the female paratype (SEABRI 2019120046) has more obvious patches on the back and a more obvious reticulated pattern on the body flanks, and the gular region is greyish white with only some tiny black spots but no stripe.

Natural history. All specimens were collected on withered leaves on the sides of small roads in forests at night while they were asleep. The collection sites are near a tributary of the Chindwin River, but there was no water body within hundreds of meters of the collection sites. There are both primary and secondary forests around the collection sites, and the woods are dense. Other reptiles also found at the site included *Bungarus fasciatus* (Schneider), *Cyrtodactylus mombergi* Grismer, Wood, Quah, Thura, Herr & Lin, *C. russelli* Bauer, *Psammodynastes pulverulentus* (Boie), and *Ptyas korros* (Schlegel).

Ptyctolaemus chindwinensis sp. nov. can change its body color within a certain range like most other draconine lizards. When they rest on withered leaves at night, their bodies are pale colored with almost no stripes or patches; when they active are on the ground during the day, their bodies become darker with obvious stripes or patches (Fig. 7). The colouration provides camouflage in their preferred habitat.

Distribution. *Ptyctolaemus chindwinensis* sp. nov. is currently only known from Htamanthi Wildlife Sanctuary, Sagaing Division, Myanmar (Fig. 8).

Comparisons. *Ptyctolaemus chindwinensis* sp. nov. can be distinguished from *P. gularis* and *Ptyctolaemus* aff. *gularis* from Tibet, China, by having relatively longer limbs (FLL/SVL 0.48–0.52 vs 0.35–0.45 in *P. gularis* and *Ptyctolaemus* aff. *gularis*, HLL/SVL 0.90–0.94 vs 0.71–0.78 in *P. gularis* and *Ptyctolaemus* aff. *gularis*), and live colorations of gular region (bright yellow with two or three short black stripes on the center of each side of the gular pouch in males and greyish white with no stripe in females vs. white with three or four long blue or bluish black stripes which occupy most portions of the gular pouch in both sexes in *Ptyctolaemus* aff. *gularis*).

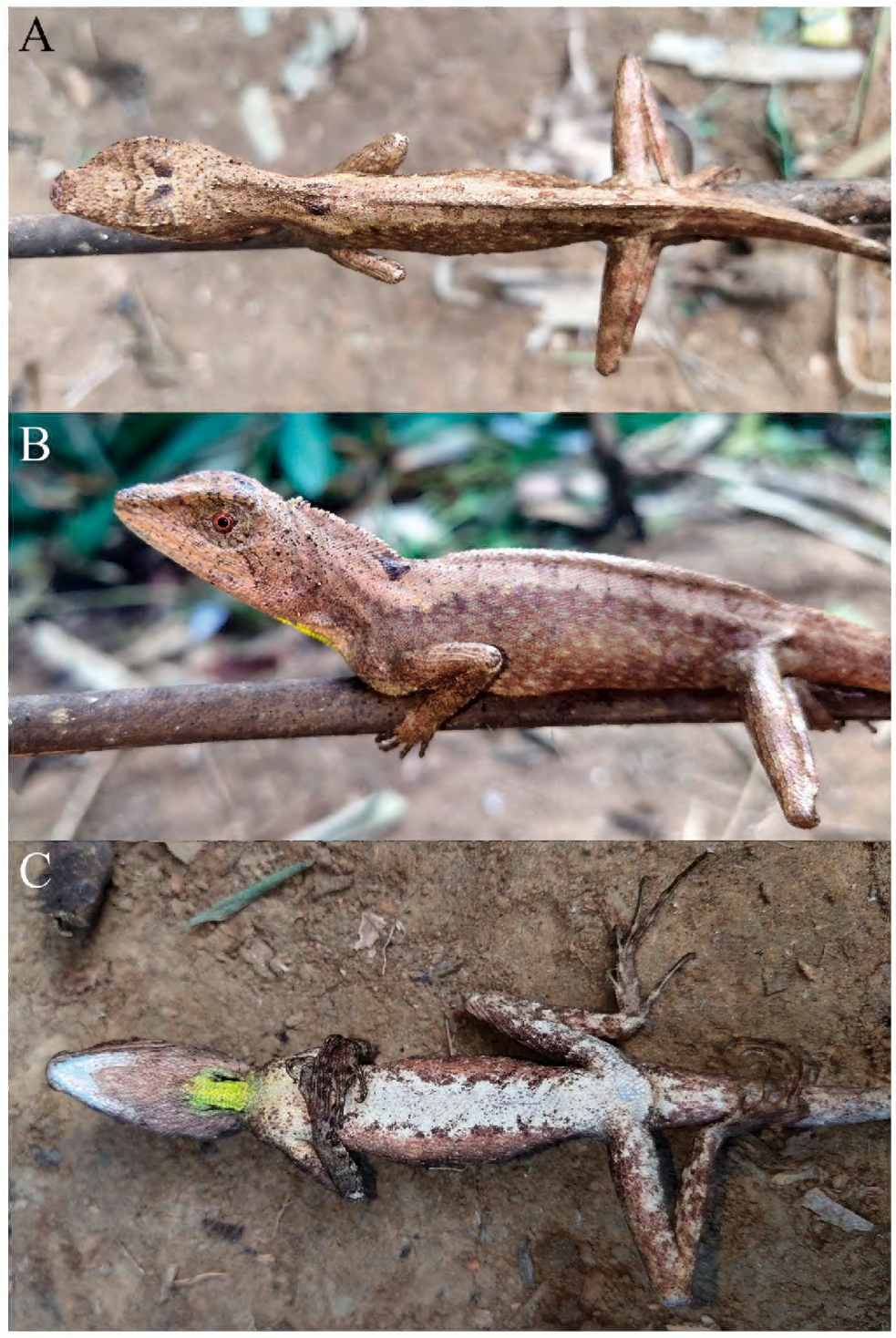

Figure 4. The holotype (SEABRI 2019120076) of *Ptyctolaemus chindwinensis* sp. nov. in life. **A.** Dorsal view; **B.** Lateral view; **C.** Ventral view.

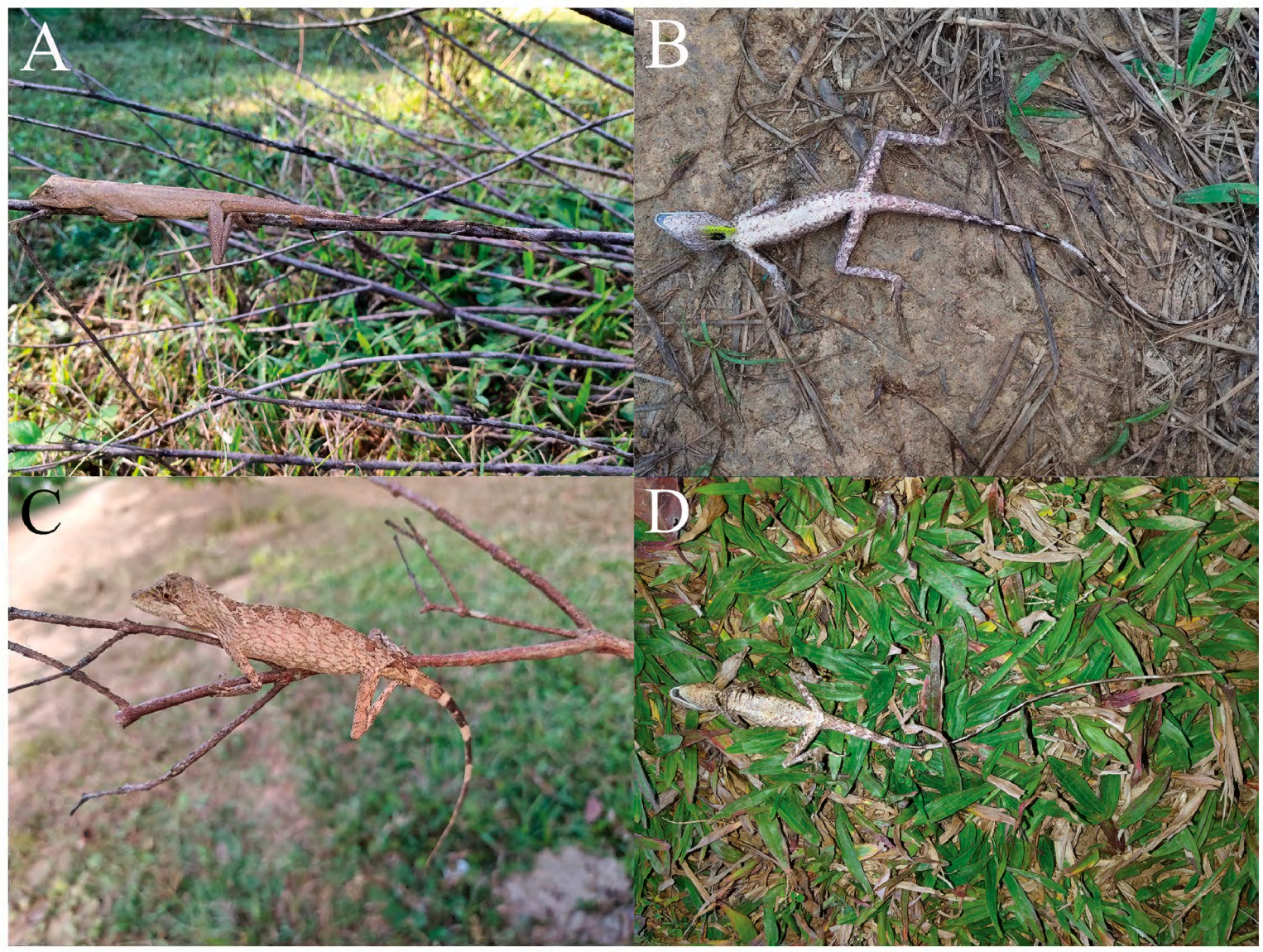

Figure 5. The adult male paratype (SEABRI 2019120031) (**A, B**) and the adult female paratype (SEABRI 2019120046) (**C, D**) of *Ptyctolaemus chindwinensis* sp. nov. in life.

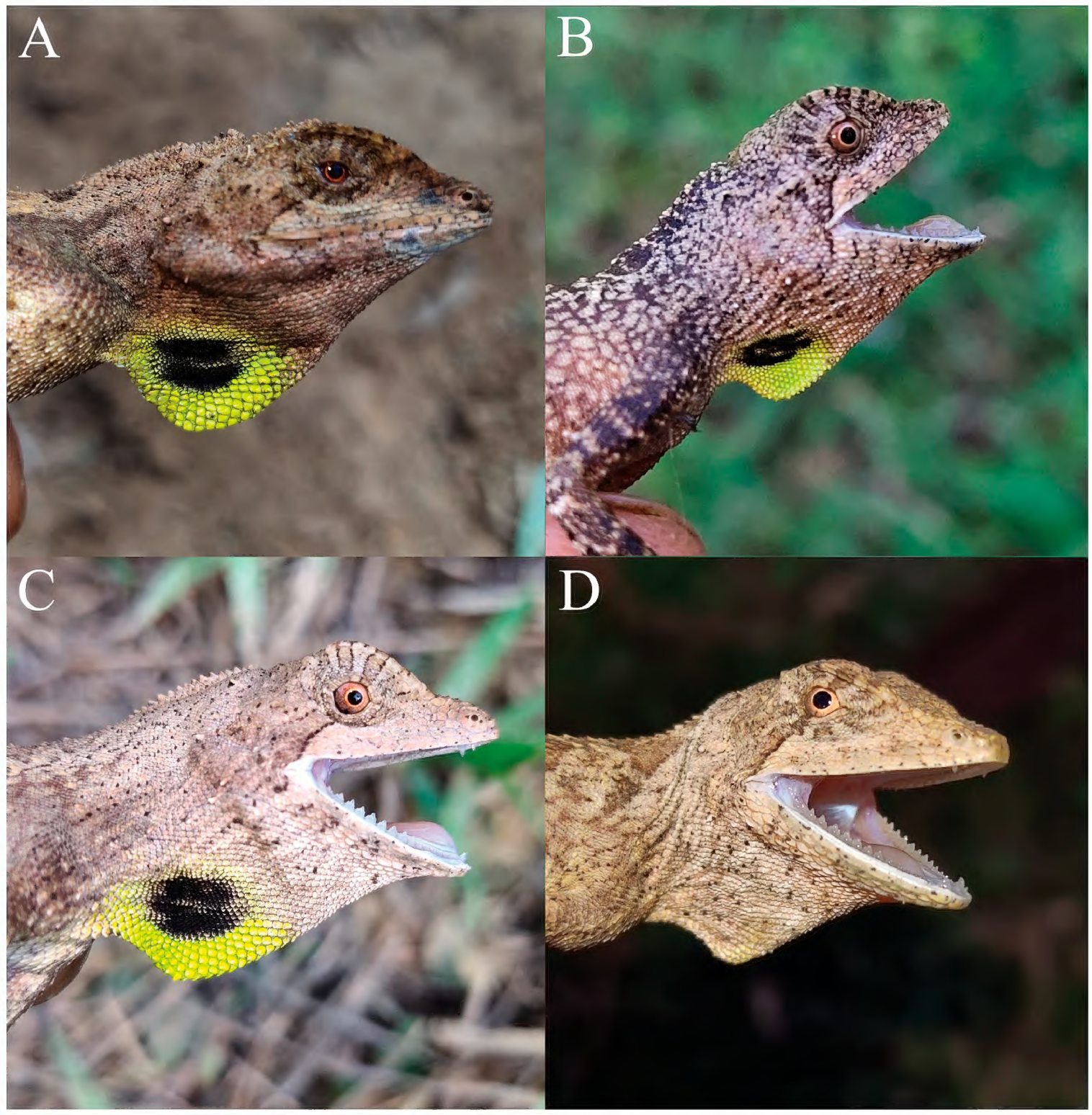

Figure 6. Close up view of the gular regions of *Ptyctolaemus chindwinensis* sp. nov. in life. **A.** The holotype (SEABRI 2019120076); **B.** The subadult male paratype (SEABRI 2019120016); **C.** The adult male paratype (SEABRI 2019120031); **D.** The adult female paratype (SEABRI 2019120046).

Table 4. Measurements (in mm) and scalation data of the type series of *Ptyctolaemus chindwinensis* sp. nov. For abbreviations see Materials and methods section.

	SEABRI 2019120076 Holotype	**SEABRI 2019120016 Paratype**	**SEABRI 2019120031 Paratype**	**SEABRI 2019120046 Paratype**
Sex	Male	Subadult male	Male	Female
SVL	83.5	45.6	76.6	65.1
TAL	206	102	182	155
TAL/SVL	2.47	2.24	2.38	2.38
HL	23.3	13.7	21.9	17.8
HW	12.8	8.6	12.5	11.0
HW/HL	0.55	0.63	0.57	0.62
HL/SVL	0.28	0.30	0.29	0.27
SEL	9.6	4.9	8.5	7.2
OD	7.2	5.1	6.7	6.7
IOD	8.8	4.9	8.0	7.3
FLL	39.8	23.8	38.7	32.5
HLL	74.8	42.3	72.3	59.5
FLL/SVL	0.48	0.52	0.51	0.50
HLL/SVL	0.90	0.93	0.94	0.91
T4L	18.0	9.5	17.0	14.5
TRL	38.4	21.4	36.9	32.1
SupL	10/11	10/10	9/10	9/9
InfL	9/10	10/10	10/10	9/8
T4S	33/35	32/31	34/32	33/34
NC	29	0	26	0
MB	105	108	113	101
VSR	73	80	69	67
VT	96	89	97	92

Figure 7. Different body colors of the subadult male paratype (SEABRI 2019120016) showed in life. **A.** On withered leaves at night; **B.** On the ground during the day.

Ptyctolaemus chindwinensis sp. nov. can be distinguished from *P. collicristatus* by having relatively longer limbs (FLL/SVL 0.48–0.52 vs 0.39–0.45 in *P. collicristatus*, HLL/SVL 0.90–0.94 vs 0.64–0.74 in *P. collicristatus*), a longer tail (TAL/SVL 2.24–2.47 vs 1.77–2.13 in *P. collicristatus*), and a lower nuchal crest in the adult males (vs. more prominent nuchal crest in adult males in *P. collicristatus*).

Discussion

In Schulte et al. (2004), there is one specimen (CAS 225592) which was identified as *Ptyctolaemus gularis*, and its collection site is very close to our new collection site, both in Htamanthi Wildlife Sanctuary, Sagaing, Myanmar. According to the morphological data of this specimen in Schulte et al. (2004), this specimen closely resembles *Ptyctolaemus chindwinensis* sp. nov. So, we consider this specimen to be conspecific with *Ptyctolaemus chindwinensis* sp. nov.

In Schulte et al. (2004), there are two specimens (USNM 123425 and BMNH 1974.846) which were also identified as *Ptyctolaemus gularis*, and their morphological characteristics are very close to *P. gularis* (Table 3). Geographically, the first specimen (USNM 123425) was collected in northeastern India, and the collection site of the second specimen (BMNH 1974.846) was given as "Myanmar, N Chengyang", but its exact location was uncertain. Through querying the website of the Natural History Museum (British Museum), we found that the voucher 1974.846 corresponds to two different collection sites, namely N'Changyong and N'Chongyong respectively. Therefore, the collection site of this specimen is uncertain. Since there are no molecular data of these two specimens, we temporarily regard these two specimens as *Ptyctolaemus* cf. *gularis*.

For the other specimens identified as *Ptyctolaemus gularis* in Schulte et al. (2004), most of which were collected

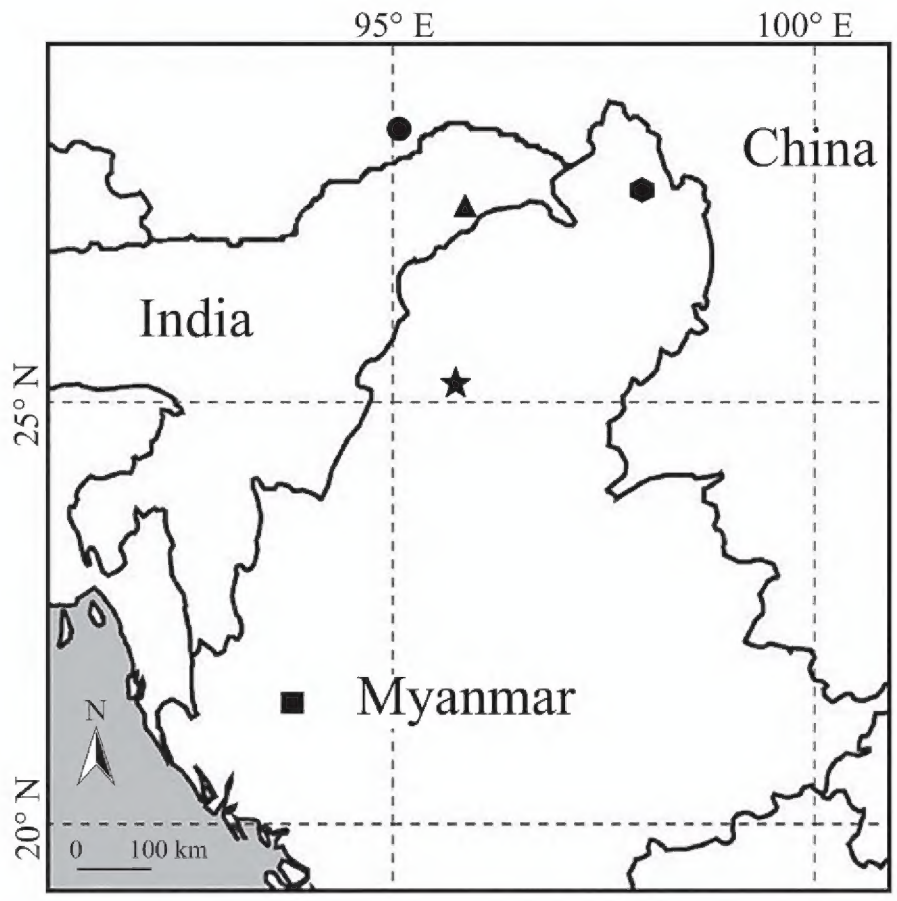

Figure 8. Map showing the type locality (star) of *Ptyctolaemus chindwinensis* sp. nov., the type locality (square) of *P. collicristatus*, the locality (dot) of *Ptyctolaemus* aff. *gularis* in Tibet, China, the locality (triangle) of *Ptyctolaemus* cf. *gularis* in northeastern India, and the locality (pentagon) of *Ptyctolaemus* sp. in Kachin, Myanmar.

from Kachin state, Myanmar. The morphological data of this specimens are close to *Ptyctolaemus chindwinensis* sp. nov., but the numbers of nuchal crest spines of these specimens are fewer than *Ptyctolaemus chindwinensis* sp. nov. (Table 3). Genetically, one sequence of a specimen (CAS 221515) from Putao, Kachin, Myanmar, and the sequences of *Ptyctolaemus chindwinensis* sp. nov. formed sister groups with strong supports (Figure 1). The average uncorrected pairwise distance (p-distance) between the sequence of the specimen (CAS 221515) from Putao, Kachin, Myanmar, and the sequences of *Ptyctolaemus chindwinensis* sp. nov. is 8.1% (Table 2). Therefore, we consider that this population in Kachin, Myanmar, represents an unnamed species.

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References

Ahmed MF, Das A, Dutta SK (2009) Amphibians and Reptiles of Northeast India - A Photographic Guide. Aaranyak, Guwahati, 122 pp.

Ahsan MF, Asmat GSM, Chakma S (2008) A Second Record of *Ptyctolaemus gularis* (Peters, 1864) from Bangladesh. Asiatic Herpetological Research 11: 10–12.

Ananjeva NB, Stuart BL (2001) The agamid lizard *Ptyctolaemus phuwuanensis* Manthey and Nabhitabhata, 1991 from Thailand and Laos represents a new genus. Russian Journal of Herpetology 8: 165–170.

Che J, Jiang K, Yan F, Zhang YP (2020) Amphibians and Reptiles in Tibet — Diversity and Evolution. Science Press, Beijing, 803 pp.

Das A, Sharma P, Harikrishnan S, Ghosh S, Nath A, Dhar D, Mondol J, Wangdi Y (2014) A Rapid Assessment of Herpetofaunal Diversity in Manas-Bhutan Transboundary Landscape. Report submitted to Field Directorate, Manas Tiger Project, Govt of Assam and Park Manager, Royal Manas National Park, Royal Government of Bhutan, Wildlife Institute of India, 38 pp.

Das A, Sharma P, Harikrishnan S, Nath A, Ghosh S, Dutta D, Mondol J, Wangdi Y (2016) Addition to the Herpetofauna of Royal Manas National Park, Bhutan, with six new country records. Herpetology Notes 9: 261–278.

Hakim J, Trageser SJ, Ghose A, Das K, Rashid SMA, Rahman SC (2020) Amphibians and reptiles from Lawachara National Park in Bangladesh. Check List 16(5): 1239–1268. https://doi.org/10.15560/16.5.1239

Hallermann J, Böhme W (2003) A reinterpretation of the agamid genus *Mantheyus* Ananjeva and Stuart, 2001, as a junior synonym of *Ptyctolaemus* Peters, 1864, with comments on the problem of monotypic genera. Hamadryad 27: 262–265.

Huang YZ (1980) A new generic record of Chinese lizard from Xizang (Tibet) — *Ptyctolaemus gularis* Peters. Acta Zootaxonomica Sinica 5: 336.

Jerdon TC (1870) Notes on Indian herpetology. Proceedings of the Asiatic Society of Bengal 3: 66–85.

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS (2017) ModelFinder: fast model selection for accurate phylogenetic estimates. Nature Methods 14: 587–589. https://doi.org/10.1038/nmeth.4285

Khandekar A, P Roy, K Kunte (2021) Reptiles of India, v. 1.25. https://www.indianreptiles.org [Accessed on 5 April 2021]

Kumar S, Stecher G, Li M, Knyaz C, Tamura K (2018) MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. Molecular Biology and Evolution 35: 1547–1549. https://doi.org/10.1093/molbev/msy096

Macey JR, Schulte JA II, Larson A, Ananjeva NB, Wang Y, Pethiyagoda R, Rastegar-Pouyani N, Papenfuss TJ (2000) Evaluating trans-tethys migration: an example using acrodont lizard phylogenetics. Systematic Biology 49(2): 233–256. https://doi.org/10.1093/sysbio/49.2.233

Manthey U, Nabhitabhata J (1991) Eine neue Agame, *Ptyctolaemus phuwuanensis* sp. n. (Sauria: Agamidae), aus Nordost-Thailand. Sauria 13: 3–6.

Manthey U (2010) Agamid Lizards of Southern Asia - Draconinae 2, Leiolepidinae. Terralog, Vol. 7b. Edition Chimaira, Frankfürt, 168 pp.

Mathew R (1995) Fauna of Meghalaya, Part I (Vertebrates, Reptilia). Zoological Survey of India, State Fauna Series 4: 379–454.

Pawar S, Birand A (2001) A Survey of Amphibians, Reptiles, and Birds in Northeast India. CERC Technical Report #6. Centre for Ecological Research and Conservation, Mysore, 118 pp.

Peters WCH (1864) Über einige neue Säugethiere (*Mormops*, *Macrotus*, *Vesperus*, *Molossus*, *Capromys*), Amphibien (*Platydactylus*,

Otocryptis, *Euprepes*, *Ungalia*, *Dromicus*, *Tropidonotus*, *Xenodon*, *Hylotes*) und Fische (*Sillago*, *Sebastes*, *Channa*, *Myctophum*, *Carassius*, *Barbus*, *Capoëta*, *Poecilia*, *Saurenchelys*, *Leptocephalus*). Monatsberichte der königlichen Akademie der Wissenschaften zu Berlin 1864: 381–399.

Purkayastha J (2013) An Amateur's Guide to Reptiles of Assam. EBH Publishers, Guwahati, 146 pp.

Purkayastha J (2018) Urban biodiversity: an insight into the terrestrial vertebrate diversity of Guwahati, India. Journal of Threatened Taxa 10(10): 12299–12316. https://doi.org/10.11609/jott.3721.10.10.12299-12316

Rambaut A, Drummond AJ, Xie D, Baele G, Suchard MA (2018) Posterior summarisation in Bayesian phylogenetics using Tracer 1.7. Systematic Biology 67(5): 901–904. https://doi.org/10.1093/sysbio/syy032

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61: 539–542. https://doi.org/10.1093/sysbio/sys029

Sambrook J, Fritsch EF, Maniatis T (1989) Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, New York, 1546 pp.

Schulte JA II, Vindum JV, Win H, Thin T, Lwin KS, Shein AK (2004) Phylogenetic relationships of the genus *Ptyctolaemus* (Squamata: Agamidae), with a description of a new species from Chin Hills of Western Myanmar. Proceedings of the California Academy of Sciences 55(12): 222–247.

Silvestro D, Michalak I (2012) raxmlGUI: a graphical front-end for RAxML. Organisms Diversity and Evolution 12(4): 335–337. https://doi.org/10.1007/s13127-011-0056-0

Smith MA (1940) The amphibians and reptiles obtained by Mr. Ronald Kaulback in upper Burma. Records of the Indian Museum 42: 465–486.

Thompson JD, Gibson TJ, Higgins DG (2002) Multiple sequence alignment using ClustalW and ClustalX. Current Protocols in Bioinformatics 00(1): 2.3.1–2.3.22. https://doi.org/10.1002/0471250953.bi0203s00

Uetz P, Freed P, Hošek J (2021) The Reptile Database. http://www.reptile-database.org [Accessed on 5 April 2021]